Amendments to the Specification:

Please replace paragraph 3 on page 4 with the following rewritten paragraph 3:

Figure 4. Amino Acid Sequences of RAFTIN1 Proteins and BURP Domains. (A) Comparison of the deduced primary structure of *RAFTIN1* gene products taRAFTIN1a (SEQ ID NO: 40), taRAFTIN1b (SEQ ID NO: 41) and osRAFTIN1 (SEQ ID NO: 43). The predicted transmembrane domains are indicated as a filled bar. The specific sequences of these regions in each gene product are boxed. (B) Alignment of BURP domains. Substitutions are shown as such: identity as hyphens, and the gaps introduced in the alignment as triangles. The highly conserved amino acids, and CH motifs are indicated as dots and stars, respectively.

Please replace paragraph 3 on page 7 with the following rewritten paragraph 3:

DNA gel blot analysis was performed to estimate the copy number of *RAFTIN1* in rice and in the allohexaploid (AABBDD genome), tetraploid (AABB) and diploid wheats (AA or DD) using the coding region of *osRAFTIN1* or *taRAFTIN1* as a probe. The *osRAFTIN1* probe hybridized to only one DNA fragment of the rice genome digested with each of 3 different restriction enzymes that do not cleave the coding region **(Figure 1B).** All recognized bands were of the sizes consistent with those obtained through electronic ~~s~~Southern analysis of the genomic sequences retrieved from the public domain (GenBank accession no: AP000364, Sasaki, T., Matsumoto, T. and Yamamoto, K., 1999). Thus, there only exists one copy of *RAFTIN1* gene in the rice genome. When the same digestion was probed with the wheat *taRAFTIN1a* ORF cDNA, the probe specifically hybridized to the DNA fragments with the same sizes as recognized by the *osRAFTIN1* probe (Figures 1B and 1C), confirming a close relationship between rice *osRAFTIN1* and wheat *RAFTIN1* genes. In wheat as shown in Figure 1C, there were 3 to 4 bands in the hexaploid (AABBDD genome), 2 in the tetraploid (AABB), 1 in one diploid (AA), and 1 to 2 in another diploid (DD). Careful comparison of the size of band(s) among different genomes strongly suggested that the *RAFTIN1* gene family was most likely represented by one copy per A or B or D complement in wheats, the isolated *taRAFTIN1a* and *taRAFTIN1b* genes were likely from the AABB genome and the related gene in DD genome might consist of one *Hind*III restriction site in the coding region resulting two hybridization bands. This assumption was partially supported by the

observation that a closely related genomic clone isolated from an AA genome wheat was closely related to *taRAFTIN1a* and the EST clone (GenBank accession no: BG274249, Anderson, O., 2001) obtained from a BB genome wheat was to *taRAFTIN1b* (data not shown).

Please replace paragraph 2 on page 9 with the following rewritten paragraph 2:

Since the *Arabidopsis* genome has been sequenced and large knockout population is available, we searched the genomic sequence for *RAFTIN1-like* genes ~~(www.arabidopsis.org)~~. BLAST analysis did not identify in the model plant any known or hypothetical genes statistically significantly homologous to *RAFTIN1* nt sequences. No overall significantly similar proteins were found in the *Arabidopsis* genome by BLASTP analyses. However, limited homology was shown between the C-terminal moiety (~200 a.a.) of *RAFTIN1* and the C-termini of 5 putative gene products, 36% identical to RD22 (a.a. 175-389) (Yamaguchi-Shinozaki & Shinozaki, 1993), 35% to an unknown protein (a.a. 86-277) (F13F21.25), 30% to an aromatic rich glycoprotein (a.a. 411-588) (F1707.9), 26% to a putative polygalacuronase isoenzyme 1 beta subunit (a.a. 311-619) (F508.31) and 27% to another polygalacturonase isoenzyme 1 beta subunit (a.a. 390-620) (T13D8.26). These conserved homologous regions were previously named BURP domain (see below). Searches for ESTs of these genes did not reveal any evidence that any EST of them was derived from anther or florescence tissues. Thus, apparently the rice and wheat anther-specific *RAFTIN1* homologues were not present in the *Arabidopsis* genome.

Please replace paragraph 1 on page 19 with the following rewritten paragraph 1:

Oligonucleotide Synthesis, DNA Sequencing and Sequence Analysis

Oligonucleotide synthesis and DNA sequencing were carried out by the DNA Technology Unit of the Plant Biotechnology Institute. DNA sequences were assembled and analyzed using Lasergene software (DNASTAR Inc., Madison, WI, USA), FASTA ~~(www.ebi.ac.uk/fasta3/)~~, BLAST 2 and BLAST ~~(www.ncbi.nlm.nih.gov)~~.

Please replace paragraph 3 on page 19 with the following rewritten paragraph 3:

RT-PCR Analysis of *RAFTIN1* Gene Expression

First strand cDNA was generated in a 20 µl reaction containing 5 µg of total RNA isolated from appropriate wheat/rice tissues, 0.5 µg oligo $(dT)_{18}$, 20 units of SUPERSCRIPT™ II RNase H⁻ Reverse Transcriptase (SUPERSCRIPT™ II Reverse Transcriptase enzyme is manufactured by Invitrogen, and is used in RT-PCR reactions for reverse transcribing mRNA.) according to the supplier's instruction. One hundred-fifty ng RNA-derived cDNA was used for a 100-µl PCR reaction in the presence of 10 units of Taq DNA polymerase (Amersham). Primers OL3044 and OL3073 (5'CTCCATGTCCACCATGTA3') (SEQ ID NO: 5) were used for amplification of an 875-bp fragment at the 5' coding region of wheat *taRAFTIN1a* cDNA, whereas primers OL3148 (5'CGACGTATTTGTCGTAGT3') (SEQ ID NO: 6) and OL3815 (5'TCTCGAACGCTTCCATG3') (SEQ ID NO: 7) were targeted at a 441-bp cDNA immediately from the putative start codon of rice *osRAFTIN1*. Primers OL4556 (5'TCGAGCTCGTCGCCGTCA3') (SEQ ID NO: 8) and OL4557 (5'GCAGCACCAGTGCTGCTG3') (SEQ ID NO: 9) binding to cDNA of a house-keeping gene, *glyceraldehyde-3-phosphate dehydrogenase* (GAPDH) were used as a control. All PCR was carried out with a Techne Genius thermocycler (Duxford, Cambridge, UK) as indicated: 35 cycles of 94°C, 30 sec; 56°C, 30 sec; and 72°C, 1 min; finally a 10-min extension at 72°C. Five µl of the reaction was used for agarose gel analysis.

Please replace paragraph 3 on page 21 with the following rewritten paragraph 3:

Promoter isolation

The upstream regulatory regions of *taRAFTIN1a* and *taRAFTIN1b* coding regions were isolated from the hexaploid wheat cultivar Karma (genetic complements: AABBDD) using a Universal GenomeWalker™ Kit (Universal GenomeWalker™ Kits are manufactured by Clontech, Palo Alto, CA and provide a polymerase chain reaction method for walking upstream or downstream in genomic DNA from a known sequence, such as an expressed sequence tag, and allows construction of libraries from the genome of any species). Two nested reverse primers, OL3070 (5'TCCAGCCTGAACCGCGACCAGGGTGGT3') (SEQ ID NO: 12) and OL3071 (5'GTGGTGGCGAGGAGGGCGACGAGGAA3') (SEQ ID NO: 13) were used for the first and second PCR. The resulting two fragments of 1.7 kb for *taRAFTIN1a* and 2.1 kb for *taRAFTIN1b* were cloned into a T/A vector (Invitrogen). The inserts were completely sequenced.